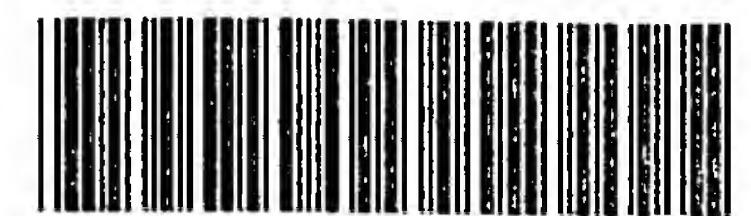


RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/591,419
Source: JFWP
Date Processed by STIC: 09/13/2006

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/591,419

DATE: 09/13/2006

TIME: 13:09:30

Input Set : N:\RJAVED\10591419.txt
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3 <110> APPLICANT: Frohberg, Claus
 4 Koetting, Oliver
 5 Ritte, Gerhard
 6 Steup, Martin
 8 <120> TITLE OF INVENTION: Methods for identifying proteins with starch phosphorylating enzymatic

9 activity
 11 <130> FILE REFERENCE: 65084.000020
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/591,419
 14 <141> CURRENT FILING DATE: 2006-09-01
 16 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/002454
 17 <151> PRIOR FILING DATE: 2005-03-04
 19 <150> PRIOR APPLICATION NUMBER: EP04090483.1
 20 <151> PRIOR FILING DATE: 2004-12-15
 22 <150> PRIOR APPLICATION NUMBER: EP04090121.7
 23 <151> PRIOR FILING DATE: 2004-03-29
 25 <150> PRIOR APPLICATION NUMBER: EP04090087.0
 26 <151> PRIOR FILING DATE: 2004-03-05
 28 <150> PRIOR APPLICATION NUMBER: US60/549,980 provisional
 29 <151> PRIOR FILING DATE: 2004-03-05
 31 <160> NUMBER OF SEQ ID NOS: 46
 33 <170> SOFTWARE: PatentIn version 3.1
 35 <210> SEQ ID NO: 1
 36 <211> LENGTH: 3591
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Arabidopsis thaliana
 40 <220> FEATURE:
 41 <221> NAME/KEY: CDS
 42 <222> LOCATION: (1)..(3591)
 43 <223> OTHER INFORMATION:

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 51 act aga aac tca tca tca ctt cct aga ctc gtt aac atc act cac 96
 52 Thr Arg Asn Ser Ser Ser Leu Pro Arg Leu Val Asn Ile Thr His
 53 20 25 30
 55 aga gtt aat ctc agc cac caa tct cac cga ctc aga aac tcc aat tct 144
 56 Arg Val Asn Leu Ser His Gln Ser His Arg Leu Arg Asn Ser Asn Ser
 57 35 40 45
 59 cgt ctc act tgc act gct act tct tcc acc att gag gaa caa cgg 192
 60 Arg Leu Thr Cys Thr Ala Thr Ser Ser Thr Ile Glu Glu Gln Arg
 61 50 55 60
 63 aag aag aaa gat gga tca gga acg aaa gtg agg ttg aat gtg agg tta 240

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PATENT APPLICATION: US/10/591,419

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68 Asp His Gln Val Asn Phe Gly Asp His Val Ala Met Phe Gly Ser Ala	
69 85 90 95	
71 aaa gag att ggt tca tgg aaa aag aaa tcg cct ttg aat tgg agt gag	336
72 Lys Glu Ile Gly Ser Trp Lys Lys Ser Pro Leu Asn Trp Ser Glu	
73 100 105 110	
75 aat gga tgg gtt tgt gag ttg gaa ctt gac ggt cag gtt ttg gag	384
76 Asn Gly Trp Val Cys Glu Leu Glu Leu Asp Gly Gly Gln Val Leu Glu	
77 115 120 125	
79 tat aag ttt gtc att gtt aag aat gat ggt tca ctt tca tgg gaa tct	432
80 Tyr Lys Phe Val Ile Val Lys Asn Asp Gly Ser Leu Ser Trp Glu Ser	
81 130 135 140	
83 ggt gat aat cgt gtc ctt aag gtt cca aat tct ggg aat ttt tct gtt	480
84 Gly Asp Asn Arg Val Leu Lys Val Pro Asn Ser Gly Asn Phe Ser Val	
85 145 150 155 160	
87 gtt tgt cat tgg gat gct act aga gaa acc ctt gat ttg cct cag gag	528
88 Val Cys His Trp Asp Ala Thr Arg Glu Thr Leu Asp Leu Pro Gln Glu	
89 165 170 175	
91 gtt ggt aat gat gat gat gtt ggt gat ggt ggg cat gag agg gat aat	576
92 Val Gly Asn Asp Asp Asp Val Gly Asp Gly Gly His Glu Arg Asp Asn	
93 180 185 190	
95 cat gat gtt ggt gat gat aga gta gtg gga agt gaa aat ggt gcg cag	624
96 His Asp Val Gly Asp Asp Arg Val Val Gly Ser Glu Asn Gly Ala Gln	
97 195 200 205	
99 ctt cag aag agt aca ttg ggt ggg caa tgg caa ggt aaa gat gcg tcc	672
100 Leu Gln Lys Ser Thr Leu Gly Gly Gln Trp Gln Gly Lys Asp Ala Ser	
101 210 215 220	
103 ttt atg cgt tct aat gat cat ggt aac aga gaa gtt ggt aga aat tgg	720
104 Phe Met Arg Ser Asn Asp His Gly Asn Arg Glu Val Gly Arg Asn Trp	
105 225 230 235 240	
107 gat act agt ggt ctt gaa ggc aca gct ctt aag atg gtt gag ggt gat	768
108 Asp Thr Ser Gly Leu Glu Gly Thr Ala Leu Lys Met Val Glu Gly Asp	
109 245 250 255	
111 cgc aac tct aag aac tgg tgg aga aag ctt gaa atg gta cgc gag gtt	816
112 Arg Asn Ser Lys Asn Trp Trp Arg Lys Leu Glu Met Val Arg Glu Val	
113 260 265 270	
115 ata gtt ggg agt gtt gag agg gag gaa cga ttg aag gcg ctc ata tac	864
116 Ile Val Gly Ser Val Glu Arg Glu Glu Arg Leu Lys Ala Leu Ile Tyr	
117 275 280 285	
119 tct gca att tat ttg aag tgg ata aac aca ggt cag att cct tgt ttt	912
120 Ser Ala Ile Tyr Leu Lys Trp Ile Asn Thr Gly Gln Ile Pro Cys Phe	
121 290 295 300	
123 gaa gat gga ggg cat cac cgt cca aac agg cat gcc gag att tcc aga	960
124 Glu Asp Gly Gly His His Arg Pro Asn Arg His Ala Glu Ile Ser Arg	
125 305 310 315 320	
127 ctt ata ttc cgt gag ttg gag cac att tgc agt aag aaa gat gct act	1008
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Input Set : N:\RJAVED\10591419.txt
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132 Pro Glu Glu Val Leu Val Ala Arg Lys Ile His Pro Cys Leu Pro Ser				
133 340	345	350		
135 ttc aaa gca gag ttt act gca gct gtc cct cta act cg	gg att agg gac			1104
136 Phe Lys Ala Glu Phe Thr Ala Ala Val Pro Leu Thr Arg Ile Arg Asp				
137 355	360	365		
139 ata gcc cat cg	aat gat att cct cat gat ctc aag caa gaa atc aag			1152
140 Ile Ala His Arg Asn Asp Ile Pro His Asp Leu Lys Gln Glu Ile Lys				
141 370	375	380		
143 cat acg ata caa aat aag ctt cac cg	gat gct ggt cca gaa gat cta			1200
144 His Thr Ile Gln Asn Lys Leu His Arg Asn Ala Gly Pro Glu Asp Leu				
145 385	390	395	400	
147 att gca aca gaa gca atg ctt caa cga att acc gag acc cca gga aaa				1248
148 Ile Ala Thr Glu Ala Met Leu Gln Arg Ile Thr Glu Thr Pro Gly Lys				
149 405	410	415		
151 tat agt gga gac ttt gtg gag cag ttt aaa ata ttc cat aat gag ctt				1296
152 Tyr Ser Gly Asp Phe Val Glu Gln Phe Lys Ile Phe His Asn Glu Leu				
153 420	425	430		
155 aaa gat ttc ttt aat gct gga agt ctc act gaa cag ctt gat tct atg				1344
156 Lys Asp Phe Phe Asn Ala Gly Ser Leu Thr Glu Gln Leu Asp Ser Met				
157 435	440	445		
159 aaa att tct atg gat gat aga ggt ctt tct gcg ctc aat ttg ttt ttt				1392
160 Lys Ile Ser Met Asp Asp Arg Gly Leu Ser Ala Leu Asn Leu Phe Phe				
161 450	455	460		
163 gaa tgt aaa aag cgc ctt gac aca tca gga gaa tca agc aat gtt ttg				1440
164 Glu Cys Lys Lys Arg Leu Asp Thr Ser Gly Glu Ser Ser Asn Val Leu				
165 465	470	475	480	
167 gag ttg att aaa acc atg cat tct cta gct tct tta aga gaa aca att				1488
168 Glu Leu Ile Lys Thr Met His Ser Leu Ala Ser Leu Arg Glu Thr Ile				
169 485	490	495		
171 ata aag gaa ctt aat agc ggc ttg cga aat gat gct cct gat act gcc				1536
172 Ile Lys Glu Leu Asn Ser Gly Leu Arg Asn Asp Ala Pro Asp Thr Ala				
173 500	505	510		
175 att gca atg cgc cag aag tgg cgc ctt tgt gag atc ggc ctc gag gac				1584
176 Ile Ala Met Arg Gln Lys Trp Arg Leu Cys Glu Ile Gly Leu Glu Asp				
177 515	520	525		
179 tac ttt gtt cta cta agc aga ttc ctc aat gct ctt gaa act atg				1632
180 Tyr Phe Phe Val Leu Leu Ser Arg Phe Leu Asn Ala Leu Glu Thr Met				
181 530	535	540		
183 gga gga gct gat caa ctg gca aaa gat gtg gga tca aga aac gtt gcc				1680
184 Gly Gly Ala Asp Gln Leu Ala Lys Asp Val Gly Ser Arg Asn Val Ala				
185 545	550	555	560	
187 tca tgg aat gat cca cta gat gct ttg gtg ttg ggt gtt cac caa gta				1728
188 Ser Trp Asn Asp Pro Leu Asp Ala Leu Val Leu Gly Val His Gln Val				
189 565	570	575		
191 ggt cta tct ggt tgg aag caa gaa gaa tgt tta gcc att gga aat gaa				1776
192 Gly Leu Ser Gly Trp Lys Gln Glu Glu Cys Leu Ala Ile Gly Asn Glu				
193 580	585	590		

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196 Leu Leu Ala Trp Arg Glu Arg Asp Leu Leu Glu Lys Glu Gly Glu Glu	
197 595 600 605	
199 gat gga aaa aca att tgg gcc atg agg ctg aaa gca act ctt gat cga	1872
200 Asp Gly Lys Thr Ile Trp Ala Met Arg Leu Lys Ala Thr Leu Asp Arg	
201 610 615 620	
203 gca cgc aga tta aca gca gaa tat tct gat ttg ctt ctt caa ata ttt	1920
204 Ala Arg Arg Leu Thr Ala Glu Tyr Ser Asp Leu Leu Leu Gln Ile Phe	
205 625 630 635 640	
207 cct cct aat gtg gag att tta gga aaa gct cta gga att cca gag aat	1968
208 Pro Pro Asn Val Glu Ile Leu Gly Lys Ala Leu Gly Ile Pro Glu Asn	
209 645 650 655	
211 agt gtc aag acc tat aca gaa gca gag att cgt gct gga att att ttc	2016
212 Ser Val Lys Thr Tyr Thr Glu Ala Glu Ile Arg Ala Gly Ile Ile Phe	
213 660 665 670	
215 cag atc tca aag ctc tgc act gtt ctt cta aaa gct gta aga aat tca	2064
216 Gln Ile Ser Lys Leu Cys Thr Val Leu Leu Lys Ala Val Arg Asn Ser	
217 675 680 685	
219 ctt ggt tct gag ggc tgg gat gtc gtt gta cct gga tcg acg tct ggg	2112
220 Leu Gly Ser Glu Gly Trp Asp Val Val Val Pro Gly Ser Thr Ser Gly	
221 690 695 700	
223 aca tta gtt cag gtt gag agc att gtt ccg gga tca ttg cca gca act	2160
224 Thr Leu Val Gln Val Glu Ser Ile Val Pro Gly Ser Leu Pro Ala Thr	
225 705 710 715 720	
227 tct ggt ggt cct att att ctc ttg gtc aat aaa gct gat ggc gat gaa	2208
228 Ser Gly Gly Pro Ile Ile Leu Leu Val Asn Lys Ala Asp Gly Asp Glu	
229 725 730 735	
231 gag gta agt gct gct aat ggg aac ata gct gga gtc atg ctt ctg cag	2256
232 Glu Val Ser Ala Ala Asn Gly Asn Ile Ala Gly Val Met Leu Leu Gln	
233 740 745 750	
235 gag ctg cct cac ttg tct cac ctt ggc gtt aga gcg cg ^g cag gag aaa	2304
236 Glu Leu Pro His Leu Ser His Leu Gly Val Arg Ala Arg Gln Glu Lys	
237 755 760 765	
239 att gtc ttt gtg aca tgt gat gat gac aag gtt gct gat ata cga	2352
240 Ile Val Phe Val Thr Cys Asp Asp Asp Asp Lys Val Ala Asp Ile Arg	
241 770 775 780	
243 cga ctt gtg gga aaa ttt gtg agg ttg gaa gca tct cca agt cat gtg	2400
244 Arg Leu Val Gly Lys Phe Val Arg Leu Glu Ala Ser Pro Ser His Val	
245 785 790 795 800	
247 aat ctg ata ctt tca act gag ggt agg agt cgc act tcc aaa tcc agt	2448
248 Asn Leu Ile Leu Ser Thr Glu Gly Arg Ser Arg Thr Ser Lys Ser Ser	
249 805 810 815	
251 gcg acc aaa aaa acg gat aag aac agc tta tct aag aaa aaa aca gat	2496
252 Ala Thr Lys Lys Thr Asp Lys Asn Ser Leu Ser Lys Lys Lys Thr Asp	
253 820 825 830	
255 aag aag agc tta tct atc gat gat gaa gaa tca aag cct ggt tcc tca	2544
256 Lys Lys Ser Leu Ser Ile Asp Asp Glu Glu Ser Lys Pro Gly Ser Ser	
257 835 840 845	
259 tct tcc aat agc ctc ctt tac tct tcc aag gat atc cct agt gga gga	2592

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/591,419

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264	Ile	Ile	Ala	Leu	Ala	Asp	Ala	Asp	Val	Pro	Thr	Ser	Gly	Ser	Lys	Ser	
265	865				870				875				880				
267	gct	gca	tgt	ggt	ctt	ctt	gca	tct	tta	gca	gaa	gcc	tct	agt	aaa	gtg	2688
268	Ala	Ala	Cys	Gly	Leu	Leu	Ala	Ser	Leu	Ala	Glu	Ala	Ser	Ser	Lys	Val	
269			885						890				895				
271	cac	agc	gaa	cac	gga	gtt	ccg	gca	tca	ttt	aag	gtt	cca	act	gga	gtt	2736
272	His	Ser	Glu	His	Gly	Val	Pro	Ala	Ser	Phe	Lys	Val	Pro	Thr	Gly	Val	
273						900			905				910				
275	gtc	ata	cct	ttt	gga	tcg	atg	gaa	tta	gct	tta	aag	caa	aat	aat	tcg	2784
276	Val	Ile	Pro	Phe	Gly	Ser	Met	Glu	Leu	Ala	Leu	Lys	Gln	Asn	Asn	Ser	
277						915			920				925				
279	gaa	gaa	aag	ttt	gcg	tct	ttg	cta	gaa	aaa	cta	gaa	acc	gcc	aga	cct	2832
280	Glu	Glu	Lys	Phe	Ala	Ser	Leu	Leu	Glu	Lys	Lys	Leu	Glu	Thr	Ala	Arg	Pro
281						930			935				940				
283	gag	ggt	ggt	gag	cta	gac	gac	ata	tgt	gac	cag	atc	cat	gaa	gtg	atg	2880
284	Glu	Gly	Gly	Glu	Leu	Asp	Asp	Ile	Cys	Asp	Gln	Ile	His	Glu	Val	Met	
285						945			950				955			960	
287	aaa	acg	ttg	caa	gtg	cct	aaa	gaa	aca	atc	aac	agc	ata	agc	aaa	gcg	2928
288	Lys	Thr	Leu	Gln	Val	Pro	Lys	Glu	Thr	Ile	Asn	Ser	Ile	Ser	Lys	Ala	
289						965			970				975				
291	ttt	ctc	aaa	gat	gct	cgt	ctc	att	gtt	cgt	tca	agt	gct	aac	gtc	gag	2976
292	Phe	Leu	Lys	Asp	Ala	Arg	Leu	Ile	Val	Arg	Ser	Ser	Ala	Asn	Val	Glu	
293						980			985				990				
295	gac	tta	gcc	gga	atg	tca	gct	gca	gga	ctc	tat	gaa	tca	atc	cct	aac	3024
296	Asp	Leu	Ala	Gly	Met	Ser	Ala	Ala	Gly	Leu	Tyr	Glu	Ser	Ile	Pro	Asn	
297						995			1000				1005				
299	gtg	agt	ccc	tcg	gat	cct	ttg	gtg	ttt	tca	gat	tcg	gtt	tgc	caa		3069
300	Val	Ser	Pro	Ser	Asp	Pro	Leu	Val	Phe	Ser	Asp	Ser	Val	Cys	Gln		
301						1010			1015				1020				
303	gtt	tgg	gct	tct	ctc	tac	aca	aga	aga	gct	gtt	cta	agc	cgt	aga		3114
304	Val	Trp	Ala	Ser	Leu	Tyr	Thr	Arg	Arg	Ala	Val	Leu	Ser	Arg	Arg		
305						1025			1030				1035				
307	gct	gct	ggt	gtc	tct	caa	aga	gaa	gct	tca	atg	gct	gtt	ctc	gtt		3159
308	Ala	Ala	Gly	Val	Ser	Gln	Arg	Glu	Ala	Ser	Met	Ala	Val	Leu	Val		
309						1040			1045				1050				
311	caa	gaa	atg	ctt	tcg	ccg	gac	tta	tca	tcc	gtt	ctg	cac	aca	gtg		3204
312	Gln	Glu	Met	Leu	Ser	Pro	Asp	Leu	Ser	Phe	Val	Leu	His	Thr	Val		
313						1055			1060				1065				
315	agt	cca	gct	gat	ccg	gac	agt	aac	ctt	gtg	gaa	gcc	gag	atc	gct		3249
316	Ser	Pro	Ala	Asp	Pro	Asp	Ser	Asn	Leu	Val	Glu	Ala	Glu	Ile	Ala		
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319	cct	ggt	tta	ggg	act	tta		gct	tca	gga	aca	aga	gga	aca	cca		3294
320	Pro	Gly	Leu	Gly	Glu	Thr	Leu	Ala	Ser	Gly	Thr	Arg	Gly	Thr	Pro		
321						1085			1090				1095				
323	tgg	aga	ctc	gct	tcg	ggt	aag	ctc	gac	ggg	att	gta	caa	acc	tta		3339
324	Trp	Arg	Leu	Ala	Ser	Gly	Lys	Leu	Asp	Gly	Ile	Val	Gln	Thr	Leu		

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/591,419

DATE: 09/13/2006
TIME: 13:09:31

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L:674 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:671
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